WHAT IS CLAIMED IS:

1. An isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of:

(a) a nucleic acid sequence that encodes a polypeptide comprising at least 7 contiguous amino acids of any one of SEQ ID NOs 4, 6, 8, and 10;

(b) a nucleic acid sequence that encodes a polypeptide comprising at least 7 contiguous amino acids of SEQ ID NO:2, wherein the isolated nucleic acid molecule is less than 15kb in size;

(c) a nucleic acid sequence that encodes a polypeptide comprising at least 9 contiguous amino acids that share 100% sequence similarity with 9 contiguous amino acids of any one of SEQ ID NOs 4, 6, 8, and 10;

(d) a nucleic acid sequence that encodes a polypeptide comprising at least 9 contiguous amino acids that share 100% sequence similarity with 9 contiguous amino acids of SEQ ID NO 2; wherein the isolated nucleic acid molecule is less than 15kb in size;

(e) at least 20 contiguous nucleotides of any of nucleotides 1-111 of SEQ ID NO:1, 1-120 of SEQ ID NO:3, 1-93 of SEQ ID NO:5, and 1-1225 of SEQ ID NO:18;

(f) a nucleic acid sequence that encodes a polypeptide comprising an amino acid sequence having at least 80% sequence similarity with a sequence selected from the group consisting of SEQ ID NO:20 and SEQ ID NO:22; and

(g) the complement of the nucleic acid of any of (a)-(f).

2. The isolated nucleic acid molecule of Claim 1 that is RNA.

3. The isolated nucleic acid molecule of Claim 1 wherein the nucleic acid sequence has at least 50% sequence identity with a sequence selected from the group consisting of any of SEQ ID NOs:1, 3, 5, 7, 9, 18, 19 and 21.

4. The isolated nucleic acid molecule of Claim 1 wherein the nucleic acid sequence encodes a polypeptide comprising an amino acid sequence selected from the group consisting of: RICSCPKRD, KICSCPKRD, RVCSCPKRD, KVCSCPKRD, RICTCPKRD, KICTCPKRD, RVCTCPKRD, KVCTCPKRD, FXCKNSC and FXCQNSC, wherein X is any amino acid.

5. The isolated nucleic acid molecule of Claim 1 wherein the nucleic acid sequence encodes at least 17 contiguous amino acids of any of SEQ ID NOs 2, 4, 6, 8, and 10.

6. The isolated nucleic acid molecule of Claim 1 wherein the nucleic acid sequence encodes a polypeptide comprising at least 19 amino acids that share 100% sequence similarity with 19 amino acids of any of SEQ ID NOs 2, 4, 6, 8, and 10.

7. The isolated nucleic acid molecule of Claim 1 wherein the nucleic acid sequence encodes a polypeptide having at least 50% sequence identity with any of SEQ ID NOs 2, 4, 6, 8, and 10.

8. The isolated nucleic acid molecule of Claim 1 wherein the nucleic acid sequence encodes at least one p53 domain selected from the group consisting of an activation domain, a DNA binding domain, a linker domain, an oligomerization domain, and a basic regulatory domain.

9. The isolated nucleic acid molecule of Claim 1 wherein the nucleic acid sequence encodes a constitutively active p53.

10. The isolated nucleic acid molecule of Claim 1 wherein the nucleic acid sequence encodes a dominant negative p53.

11. ~~A vector comprising the nucleic acid molecule of Claim 1.~~

12. A host cell comprising the vector of Claim 11.

13. A process for producing a p53 polypeptide comprising culturing the host cell of Claim 8 under conditions suitable for expression of the p53 polypeptide and recovering the polypeptide.

14. A purified polypeptide comprising an amino acid sequence selected from the group consisting of:

a) at least 7 contiguous amino acids of any one of SEQ ID NOs 2, 4, 6, 8, and 10;

b) at least 9 contiguous amino acids that share 100% sequence similarity with at least 9 contiguous amino acids of any one of SEQ ID NOs 2, 4, 6, 8, and 10; and

c) at least 10 contiguous amino acids of a sequence selected from the group consisting of SEQ ID NO:20 and SEQ ID NO:22.

15. The purified polypeptide of Claim 14 wherein the amino acid sequence is selected from the group consisting of RICSCPKRD, KICSCPKRD, RVCSCPKRD, KVCSCPKRD, RICTCPKRD, KICTCPKRD, RVCTCPKRD, KVCTCPKRD, FXCKNSC and FXCQNSC, wherein X is any amino acid.

16. The purified polypeptide of Claim 14 wherein the amino acid sequence has at least 50% sequence similarity with a sequence selected from the group consisting of SEQ ID NOs 2, 4, 6, 8, and 10.

17. A method for detecting a candidate compound or molecule that modulates p53 activity said method comprising contacting a p53 polypeptide, or a nucleic acid encoding the p53 polypeptide, with one or more candidate compounds or molecules, and detecting any interaction between the candidate compound or molecule and the p53 polypeptide or nucleic acid; wherein the p53 polypeptide comprises an amino acid sequence selected from the group consisting of:

a) at least 7 contiguous amino acids of any one of SEQ ID NOs 2, 4, 6, 8, and 10; and

b) at least 9 contiguous amino acids that share 100% sequence similarity with at least 9 contiguous amino acids of any one of SEQ ID NOs 2, 4, 6, 8, and 10.

18. The method of Claim 17 wherein the candidate compound or molecule is a putative pharmaceutical agent.

19. The method of Claim 17 wherein the contacting comprises administering the candidate compound or molecule to cultured host cells that have been genetically engineered to express the p53 protein.

20. The method of Claim 17 wherein the contacting comprises administering the candidate compound or molecule to an insect has been genetically engineered to express the p53 protein.

21. The method of Claim 20 wherein the candidate compound is a putative pesticide.

22. A first insect that has been genetically modified to express or mis-express a p53 protein, or the progeny of the insect that has inherited the p53 protein expression or mis-expression, wherein the p53 protein comprises an amino acid sequence selected from the group consisting of:

a) at least 7 contiguous amino acids of any one of SEQ ID NOs 2, 4, 6, 8, and 10; and

b) at least 9 contiguous amino acids that share 100% sequence similarity with at least 9 contiguous amino acids of any one of SEQ ID NOs 2, 4, 6, 8, and 10.

23. The insect of Claim 22 wherein said insect is *Drosophila* that has been genetically modified to express a dominant negative p53 having a mutation selected from the group consisting of R155H, H159N, and R266T.

24. A method for studying p53 activity comprising detecting the phenotype caused by the expression or mis-expression of the p53 protein in the first insect of Claim 22.

25. The method of Claim 24 additionally comprising observing a second insect having the same genetic modification as the first insect which causes the expression or mis-expression of the p53 protein, and wherein the second animal additionally comprises a mutation in a gene of interest, wherein differences, if any, between the phenotype of the first animal and the phenotype of the second animal identifies the gene of interest as capable of modifying the function of the gene encoding the p53 protein.

26. The method of Claim 24 additionally comprising administering one or more candidate compounds or molecules to the insect or its progeny and observing any changes in p53 activity of the insect or its progeny.

27. A method of modulating p53 activity comprising contacting an insect cell with the isolated nucleic acid molecule of claim 1, wherein the isolated nucleic acid molecule is dsRNA derived from a coding region of a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, 3, 5, 7, and 9.

28. The method of Claim 27 wherein cultured insect cells are contacted with the dsRNA and apoptosis of the cultured cells is assayed.